

SCORE Search Results Details for Application 10521049 and Search Result 20071113_120427_us-10-521-049-12.rng.

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GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: November 13, 2007, 12:10:03 ; Search time 1016 Seconds
(without alignments)
4595.135 Million cell updates/sec

Title: US-10-521-049-12
Perfect score: 630
Sequence: 1 atcgccacaccgcggggagc.....agacagaccacggggcgagg 630

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_200701:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

16: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	630	100.0	630	12	ADI81791	Adi81791 Human tau
2	630	100.0	702	12	ADI81790	Adi81790 Human tau
3	630	100.0	720	12	ADI81793	Adi81793 Human tau
4	630	100.0	792	12	ADI81792	Adi81792 Human tau
5	630	100.0	876	12	ADI81789	Adi81789 Human tau
6	630	100.0	1059	2	AAT69790	Aat69790 Human tau
7	630	100.0	1059	2	AAX75754	Aax75754 Human mic
8	630	100.0	1107	3	AAZ29262	Aaz29262 Human Tau
9	630	100.0	1108	6	ABK83763	Abk83763 Human cDN
10	630	100.0	1108	15	AEE60794	Aee60794 Human pat
11	630	100.0	1108	15	AEF92680	Aef92680 Human Tau
12	630	100.0	1108	15	AEG70585	Aeg70585 Human p53
13	630	100.0	1233	15	AEL56834	Ael56834 Human mic
14	630	100.0	2174	15	AEL56822	Ael56822 Human mic
15	630	100.0	2308	15	AEL56824	Ael56824 Human mic
16	630	100.0	2529	6	ABQ80742	Abq80742 Human Tau
17	630	100.0	2529	14	ADV42372	Adv42372 Human Tau
18	630	100.0	2529	14	ADU82408	Adu82408 Human Tau
19	630	100.0	2529	14	ADV86197	Adv86197 Human bra
20	630	100.0	2529	14	ADV51196	Adv51196 Human Tau
21	630	100.0	2529	14	ADZ88275	Adz88275 Human tau
22	630	100.0	2529	14	ADZ85405	Adz85405 Human Tau
23	630	100.0	2529	14	AEA37348	Aea37348 Human Tau
24	630	100.0	2529	14	AEA37361	Aea37361 Human Tau
25	630	100.0	2529	14	AEA37374	Aea37374 Human Tau
26	630	100.0	2529	14	AEA37387	Aea37387 Human Tau
27	626.8	99.5	1107	1	AAN91707	Aan91707 Paired he

SCORE Search Results Details for Application 10521049 and Search Result 20071113_120428_us-10-521-049-12.rge.

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OM nucleic - nucleic search, using sw model

Run on: November 13, 2007, 12:04:43 ; Search time 10186 Seconds
(without alignments)
4275.063 Million cell updates/sec

Title: US-10-521-049-12
Perfect score: 630
Sequence: 1 atcgccacaccgcggggagc.....agacagaccacggggcgag 630

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	630	100.0	630	2	CQ768352	CQ768352 Sequence
2	630	100.0	630	2	DD261347	DD261347 Transgeni
3	630	100.0	702	2	CQ768351	CQ768351 Sequence
4	630	100.0	702	2	DD261346	DD261346 Transgeni
5	630	100.0	720	2	CQ768354	CQ768354 Sequence
6	630	100.0	720	2	DD261349	DD261349 Transgeni
7	630	100.0	792	2	CQ768353	CQ768353 Sequence
8	630	100.0	792	2	DD261348	DD261348 Transgeni
9	630	100.0	876	2	CQ768350	CQ768350 Sequence
10	630	100.0	876	2	DD261345	DD261345 Transgeni
11	630	100.0	1059	2	A62328	A62328 Sequence 16
12	630	100.0	1059	2	A62330	A62330 Sequence 18
13	630	100.0	1059	2	A62332	A62332 Sequence 20
14	630	100.0	1059	2	AR075561	AR075561 Sequence
15	630	100.0	1059	2	BD084809	BD084809 Diagnosis
16	630	100.0	1059	5	BT006772	BT006772 Homo sapi
17	630	100.0	1059	8	AY889347	AY889347 Synthetic
18	630	100.0	1059	8	AY889348	AY889348 Synthetic
19	630	100.0	1059	8	AY891838	AY891838 Synthetic
20	630	100.0	1059	8	BT007911	BT007911 Synthetic
21	630	100.0	1107	2	I17644	I17644 Sequence 1
22	630	100.0	1108	2	A08372	A08372 Synthetic n
23	630	100.0	1108	2	CS239175	CS239175 Sequence
24	630	100.0	1108	5	HUMTAUA	J03778 Human micro
25	630	100.0	1173	2	AR030346	AR030346 Sequence
26	630	100.0	1173	2	AR062941	AR062941 Sequence
27	630	100.0	1391	5	BC000558	BC000558 Homo sapi
28	630	100.0	2252	5	BC099721	BC099721 Homo sapi
29	630	100.0	2252	5	BC101936	BC101936 Homo sapi
30	630	100.0	2253	5	BC098281	BC098281 Homo sapi
31	630	100.0	2254	5	BC114504	BC114504 Homo sapi
32	630	100.0	2527	2	CQ723152	CQ723152 Sequence
33	630	100.0	2529	2	AX522066	AX522066 Sequence
34	630	100.0	6794	5	AK226139	AK226139 Homo sapi
35	628.4	99.7	1173	2	AR152002	AR152002 Sequence
36	625.2	99.2	732	5	AY526356	AY526356 Homo sapi
37	609.8	96.8	748	5	AY369830	AY369830 Pan trogl
38	592.2	94.0	3122	5	AK095802	AK095802 Homo sapi
39	579.4	92.0	1059	5	S83356	S83356 {pseudogene
40	527	83.7	723	2	CQ768343	CQ768343 Sequence
41	527	83.7	723	2	DD261338	DD261338 Transgeni
42	527	83.7	795	2	CQ768342	CQ768342 Sequence
43	527	83.7	795	2	DD261337	DD261337 Transgeni
44	527	83.7	813	2	CQ768345	CQ768345 Sequence
45	527	83.7	813	2	DD261340	DD261340 Transgeni